

SEQUENCE LISTING

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<120> Protein-Protein Interactions

<130> 1318-290-II

<150> US 60/259,572

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<160> 4

<170> PatentIn version 3.0

<210> 1

<211> 40

<212> DNA

<213> Artificial

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<221> oligonucleotide primer

<400> 1

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<210> 1

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<221> oligonucleotide primer

<400> 1

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39

<210> 1

<211> 1633

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (152)..(1633)

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atgtgtgagc agacagccac cgagggccga aattctgagc ttctctctgg aaccaggcag

120

gagacataca gacaagaaaag gcaaaattcac c atg gcc tcc acc aat gca gag

180

Met Ala Ser Thr Asn Ala Glu

1

5

agg cag ctg cag aga atc atc cga gac ttg caa gat gat gtc aca gaa

240

Ser Gln Leu Gln Arg Ile Ile Arg Asp Leu Gln Asp Ala Val Thr Glu

10

15

20

cta agc aaa gaa ttt cag gaa gca ggg gaa ccc att atg gat gac agc

260

Leu Ser Lys Glu Phe Gln Glu Ala Gly Glu Pro Ile Thr Asp Asp Ser

25

30

35

acc agc ttg cat aaa ttt tct tat aaa att gag tat ctc ctg caa ttt Thr Ser Leu His Lys Phe Ser Tyr Lys Leu Gln Tyr Leu Leu Gln Phe 45 45 50 55	316
gat cag aaa gag aag gcc acc ctc ctg ggc aac aag aag gac tac tgg Asp Gln Lys Glu Lys Ala Thr Leu Leu Gly Asn Lys Lys Asp Tyr Trp 60 65 70	364
gat tac ttc tgt gcc tgc ctg gcc aag gtg aaa gga gcc aat gat ggg Asp Tyr Phe Cys Ala Cys Leu Ala Lys Val Lys Gly Ala Asn Asp Gly 75 80 85	412
atc cgc ttt gtc aag tct atc tca gag ctc cga aca tcc ttg ggg aaa Ile Arg Phe Val Lys Ser Ile Ser Glu Leu Arg Thr Ser Leu Gly Lys 90 95 100	460
gga aga gca ttt att cgc tac tcc ttg gtg caa cag agg ttg gca gac Gly Arg Ala Phe Ile Arg Tyr Ser Leu Val His Gln Arg Leu Ala Asp 105 110 115	508
acc tta cag cag tgc ttc atg aac acc aaa gtg acc agt gac tgg tac Thr Leu Gln Gln Cys Phe Met Asn Thr Lys Val Thr Ser Asp Trp Tyr 120 125 130 135	556
tat gca aga agc ccc ttt ctg cag cca aag ctg agc tcc gac att gtg Tyr Ala Arg Ser Pro Phe Leu Gln Pro Lys Leu Ser Ser Asp Ile Val 140 145 150	604
ggc caa ctc tat gag ctg act gag gtt cag ttt gac ctg ggc tcc agg Gly Gln Leu Tyr Glu Leu Thr Glu Val Gln Phe Asp Leu Ala Ser Arg 155 160 165	652
ggc ttt gac ttg gat gct gcc tgg cca aca ttt gcc agg agg acg ctg Gly Phe Asp Leu Asp Ala Ala Trp Pro Thr Phe Ala Arg Arg Thr Leu 170 175 180	700
acc act ggc tct tct gct tac ctg tgg aaa ccc cct agc cgc agc tcc Thr Thr Gly Ser Ser Ala Tyr Leu Trp Lys Pro Pro Ser Arg Ser Ser 185 190 195	748
agc atg agc agc ttg gtg agc agc tac ctg cag act caa gag atg gtg Ser Met Ser Ser Leu Val Ser Ser Tyr Leu Gln Thr Gln Glu Met Val 200 205 210 215	796
tcc aac ttt gac ctg aac agc ccc cta aac aac gag gca ttg gag ggc Ser Asn Phe Asp Leu Asn Ser Pro Leu Asn Asn Glu Ala Leu Glu Gly 220 225 230	844
ttt gat gag atg cga cta gag ctg gac cag ttg gag gtd cgg gag aag Phe Asp Glu Met Arg Leu Glu Leu Asp Gln Leu Glu Val Arg Glu Lys 235 240 245	892
cag cta cgg gag cgc atg cag cag ctg gac aga gag aac cag gag ctg Gln Leu Arg Glu Arg Met Gln Gln Leu Asp Arg Glu Asn Gln Glu Leu 250 255 260	940
agg gca gct gtc agc cag caa ggg gag caa ctg cag aca gag agg gag Arg Ala Ala Val Ser Gln Gln Gly Glu Gln Leu Thr Glu Arg Glu 265 270 275	988
agg ygg cgg act gca ggg gag gac aac gtt cgg ctc act tgc ttg gta Arg Gly Arg Thr Ala Ala Gln Asp Asn Val Arg Leu Thr Cys Leu Val 280 285 290	1036

gat gag ttc cag aag cag tgg gag gtc att gag ggc att cag aac act 1084
 Ala Glu Leu Gln Lys Gln Trp Glu Val Thr Gln Ala Thr Gln Asn Thr
 309 305 310

gtg aag gag ctg cag aca tgc ctg cag ggc ctg gag cta gga gca gca 1132
 Val Lys Glu Leu Gln Thr Cys Leu Gln Gly Leu Glu Leu Gly Ala Ala
 315 320 325

gag aag gag gag gac tac cac aca gcc ctg cgg cgg ctg gag tcc atg 1180
 Glu Lys Glu Glu Asp Tyr His Thr Ala Leu Arg Arg Leu Glu Ser Met
 330 335 340

ctg cag ccc ttg gca cag gag ctt gag gcc aca cgg gac tca ctg gac 1228
 Leu Gln Pro Leu Ala Gln Glu Leu Glu Ala Thr Arg Asp Ser Leu Asp
 345 350 355

aag aaa aac cag cat tta gcc agc ttc cca ggc tgg cta gcc atg gct 1276
 Lys Lys Asn Gln His Leu Ala Ser Phe Pro Gly Trp Leu Ala Met Ala
 360 365 370 375

cag cag aag gca gat acg gca tca gac aca aag ggc cgg caa gaa cct 1324
 Gln Gln Lys Ala Asp Thr Ala Ser Asp Thr Lys Gly Arg Gln Glu Pro
 380 385 390

att ccc agt gat ggc gcc cag gag atg cag gag cta ggg gag aag ctt 1372
 Ile Pro Ser Asp Ala Ala Gln Glu Met Gln Glu Leu Gly Glu Lys Leu
 395 400 405

caa gcc cta gaa agg gag aga acc aag gtc gag gag gtc aac aga cag 1420
 Gln Ala Leu Glu Arg Glu Arg Thr Lys Val Glu Glu Val Asn Arg Gln
 410 415 420

cag agt gcc caa ctg gaa cag ctg gtc aag gag ctt cag ctg aaa gag 1468
 Gln Ser Ala Gln Leu Glu Gln Leu Val Lys Glu Leu Gln Leu Lys Glu
 425 430 435

gat gcc cgg gcc agc ctg gag cgc ctg gtc aag gag atg gcc cca ctc 1516
 Asp Ala Arg Ala Ser Leu Glu Arg Leu Val Lys Glu Met Ala Pro Leu
 440 445 450 455

cag gag gag ttg tct ggg aag gga cag gag gca gac cag ctc tgg cga 1564
 Gln Glu Glu Leu Ser Gly Lys Gly Gln Glu Ala Asp Gln Leu Trp Arg
 460 465 470

cgg ctg cag gag ttg ctg gcc cac acg agc tcc tgg gag gag gag cta 1612
 Arg Leu Gln Glu Leu Leu Ala His Thr Ser Ser Trp Glu Glu Glu Leu
 475 480 485

gca gag ttg agg cgg gag aaa 1633
 Ala Glu Leu Arg Arg Glu Lys
 490

<210> 4
 <211> 494
 <212> PRT
 <213> Homo sapiens

<400> 4
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 Leu Gln Asp Ala Val Thr Glu Leu Ser Lys Glu Phe Gln Glu Ala Gly
 20 25 30

Glu	Pro	Ile	Thr	Asp	Asp	Ser	Thr	Ser	Leu	His	Lys	Phe	Ser	Tyr	Lys	35	40	45
Leu	Glu	Tyr	Leu	Leu	Gln	Phe	Asp	Gln	Lys	Gln	Lys	Ala	Thr	Leu	Leu	50	55	60
Gly	Asn	Lys	Lys	Asp	Tyr	Trp	Asp	Tyr	Phe	Cys	Ala	Cys	Leu	Ala	Lys	65	70	75
Val	Lys	Gly	Ala	Asn	Asp	Gly	Ile	Arg	Phe	Val	Lys	Ser	Ile	Ser	Glu	85	90	95
Leu	Arg	Thr	Ser	Leu	Gly	Lys	Gly	Arg	Ala	Phe	Ile	Arg	Tyr	Ser	Leu	100	105	110
Val	His	Gln	Arg	Leu	Ala	Asp	Thr	Leu	Gln	Gln	Cys	Phe	Met	Asn	Thr	115	120	125
Lys	Val	Thr	Ser	Asp	Trp	Tyr	Tyr	Ala	Arg	Ser	Pro	Phe	Leu	Gln	Pro	130	135	140
Lys	Leu	Ser	Ser	Asp	Ile	Val	Gly	Gln	Leu	Tyr	Glu	Leu	Thr	Glu	Val	145	150	155
Gln	Phe	Asp	Leu	Ala	Ser	Arg	Gly	Phe	Asp	Leu	Asp	Ala	Ala	Trp	Pro	165	170	175
Thr	Phe	Ala	Arg	Arg	Thr	Leu	Thr	Thr	Gly	Ser	Ser	Ala	Tyr	Leu	Trp	180	185	190
Lys	Pro	Pro	Ser	Arg	Ser	Ser	Ser	Met	Ser	Ser	Leu	Val	Ser	Ser	Tyr	195	200	205
Leu	Gln	Thr	Gln	Glu	Met	Val	Ser	Asn	Phe	Asp	Leu	Asn	Ser	Pro	Leu	210	215	220
Asn	Asn	Glu	Ala	Leu	Glu	Gly	Phe	Asp	Glu	Met	Arg	Leu	Glu	Leu	Asp	225	230	235
Gln	Leu	Glu	Val	Arg	Glu	Lys	Gln	Leu	Arg	Glu	Arg	Met	Gln	Gln	Leu	245	250	255
Asp	Arg	Glu	Asn	Gln	Glu	Leu	Arg	Ala	Ala	Val	Ser	Gln	Gln	Gly	Glu	260	265	270
Gln	Leu	Gln	Thr	Glu	Arg	Glu	Arg	Gly	Arg	Thr	Ala	Ala	Glu	Asp	Asn	275	280	285
Val	Arg	Leu	Thr	Cys	Leu	Val	Ala	Glu	Leu	Gln	Lys	Gln	Trp	Glu	Val	290	295	300
Thr	Gln	Ala	Thr	Gln	Asn	Thr	Val	Lys	Glu	Leu	Gln	Thr	Cys	Leu	Gln	305	310	315
Gly	Leu	Glu	Leu	Gly	Ala	Ala	Glu	Lys	Glu	Glu	Asp	Tyr	His	Thr	Ala	325	330	335
Leu	Arg	Arg	Leu	Glu	Ser	Met	Leu	Gln	Pro	Leu	Ala	Gln	Glu	Leu	Glu	340	345	350
Ala	Thr	Arg	Asp	Ser	Leu	Asp	Lys	Lys	Asn	Gln	His	Leu	Ala	Ser	Phe	355	360	365

Pro Gly Trp Leu Ala Met Ala Gln Gln Lys Ala Asp Thr Ala Ser Asp
370 375 380

Thr Lys Gly Arg Gln Glu Pro Ile Pro Ser Asp Ala Ala Gln Glu Met
385 390 395 400

Gln Glu Leu Gly Glu Lys Leu Gln Ala Leu Glu Arg Glu Arg Thr Lys
405 410 415

Val Glu Glu Val Asn Arg Gln Gln Ser Ala Gln Leu Glu Gln Leu Val
420 425 430

Lys Glu Leu Gln Leu Lys Glu Asp Ala Arg Ala Ser Leu Glu Arg Leu
435 440 445

Val Lys Glu Met Ala Pro Leu Gln Glu Glu Leu Ser Gly Lys Gly Gln
450 455 460

Glu Ala Asp Gln Leu Trp Arg Arg Leu Gln Glu Leu Leu Ala His Thr
465 470 475 480

Ser Ser Trp Glu Glu Glu Leu Ala Glu Leu Arg Arg Glu Lys
485 490